A.

SEQ ID NO:1

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121   tttttggaag cgcatcgagc tgaattaacg aatgctatga ttgatgaaga cttaaatgtg
181   ttacaagagt ataaagatca acaaaaacat tatgacggtc ataaatttgc tgattgtcca
241   aatttcgtaa aggggcatgt gcctgagtta tatgttgata ataaccgaat taaaatacgc
301   tatttacaat gcccatgtaa aatcaagtac gacgaagaac gctttgaagc tgagctaatt
361   acatctcatc atatgcaacg agatacttta aatgccaaat gaaagatat  ttatatgaat
421   catcgagacc gtcttgatgt agctatggca gcagatgata tttgtacagc aataactaat
481   ggggaacaag tgaaaggcct ttacctttat ggtccatttg gacaggtaa atcttttatt
541   ctaggtgcaa ttgcgaatca gctcaaatct aagaaggtac gttcgacaat tatttatta
601   ccggaattta ttagaacatt aaaaggtggc tttaaagatg gttctttga aaagaaatta
661   catcgcgtaa gagaagcaaa cattttaatg cttgatgata ttggggctga agaagtgact
721   ccatgggtga gagatgaggt aattggacct ttgctacatt atcgaatggt tcatgaatta
781   ccaacattct ttagttctaa ttttgactat agtgaattgg aacatcattt agcgatgact
841   cgtgatggtg aagagaagac taaagcagca cgtattattg aacgtgtcaa atctttgtca
901   acaccatact ttttatcagg agaaaatttc agaaacaatt ga
```

B.

SEQ ID NO:2

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1     MGGGQSIMKQ FKSIINTSQD FEKRIEKIKK EVINDPDVKQ FLEAHRAELT NAMIDEDLNV
61    LQEYKDQQKH YDGHKFADCP NFVKGHVPEL YVDNNRIKIR YLQCPCKIKY DEERFEAELI
121   TSHHMQRDTL NAKLKDIYMN HRDRLDVAMA ADDICTAITN GEQVKGLYLY GPFGTGKSFI
181   LGAIANQLKS KKVRSTIIYL PEFIRTLKGG FKDGSFEKKL HRVREANILM LDDIGAEEVT
241   PWVRDEVIGP LLHYRMVHEL PTFFSSNFDY SELEHHLAMT RDGEEKTKAA RIIERVKSLS
301   TPYFLSGENF RNN
```

Fig. 1

SEQ ID NO : 3

Complete genome sequence of bacteriophage 77

```
1      gatcaaaata cttggggaac ggttagggag taaacttcgc gataattta aaaattcatg
61     tataaccccc ctcttataac catttaagg caggtgatga aatggagatt atagtcgatg
121    aaaatttagt gcttaaagaa aaagaaaggc tacaagtatt atataaagac atacctagca
181    ataaattaaa agtagttgat ggtttaatta ttcaagcagc aaggctacgt gtaatgcttg
241    attacatgtg ggaagacata aaagaaaaag gtgattatga tttatttact caatctgaaa
301    aggcgccacc atatgaaagg gaaagaccag tagccaaact atttaatgct agagatgctg
361    catatcaaaa aataatcaaa caattatcgg atttattgcc cgaagagaaa gaagacacag
421    aaacgccatc tgatgattac ctatgattag taataaatac gttgatgaat atataaattt
481    gtggaaacaa ggaaagataa ttttaaataa agaaagaatt gatctcttta attatctaca
541    aaaacatata tattcacgag atgatgtata ttttgatgaa cagaaaatcg aggattgtat
601    caaatttatt gaaaaatggt attttccaac attaccattt caaaggttta tcatagctaa
661    tatatttctt atagataaaa atacagatga agctttcttt acagaatttg ctattttcat
721    gggacgtgga ggcgggaaaa acggtctaat aagtgctatt agtgattttc tttctacgcc
781    cttacacgga gttaaagaat atcacatctc cattgttgct aatagtgaag atcaagcaaa
841    aacatcgttt gatgaaatca gaaccgtttt aatggataac aaacgaaata agacgggtaa
901    aacgccaaaa gctccttatg aagttagtaa agcaaaaata ataaccgtg caactaaatc
961    ggttattcga tataacacat caaacacaaa aaccaaagac ggtggacgtg aggggtgtgt
1021   tattttgat gaaattcatt atttctttgg tcctgaaatg gtaaacgtca aacgtggtgg
1081   attaggtaaa aagaaaaata gaagaacgtt ttatataagt actgatggtt ttgttagaga
1141   gggttatatc gatgcaatga agcacaaaat tgcaagtgta ttaagtggca aggttaaaaa
1201   tagtagattg tttgcttttt attgtaagtt agacgatcca aaagaagttg atgacagaca
1261   gacgtgggaa aaggcgaacc caatgttaca taaaccgtta tcagaatacg ctaaaacact
1321   gctaagcacg attgaagaag aatataacga tttaccattc aaccgttcaa ataagcccga
1381   attcatgact aagcgaatga atttgcctga agttgacctt gaaaaagtaa tagcaccatg
1441   gaaagaaata ctagcgacta atagagagat accaaattta gataatcaaa tgtgtattgg
1501   tggtttagac tttgcaaaca ttcgagattt tgcaagtgta gggctattat tccgaaaaaa
1561   cgatgattac atttggttag gacattcgtt tgtaagacaa gggtttttgg atgatgtcaa
1621   attagaacct cctattaaag aatgggaaaa aatgggatta ttgaccattg tcgatgatga
1681   tgtcattgaa attgaatata tagttgattg gttttaaag gctagagaaa aatatgggct
1741   tgaaaaagtc atagctgata attatagaac tgatattgta agacgtgcgt ttgaggatgc
1801   tggcataaaa cttgaagtac ttagaaatcc aaaagcaata catggattac ttgcaccacg
1861   tatcgataca atgtttgcga aacataacgt aatatatgga gacaatcctt tgatgcgttg
1921   gttactaat aatgttgctg taaaaatcaa gccggatgga aataaagagt atatcaaaaa
1981   agatgaagtc agacgtaaaa cggatggatt catggctttt gttcacgcat tatatagagc
2041   agacgatata gtagacaaag acatgtctaa agcgcttgat gcattaatga gtatagattt
2101   ctaatagagg aggtgagaca tgagtattct agaaaagata tttaaaacta ggaaagatat
2161   aacatatatg cttgatttag atatgataga agatctatca caacaagcgt atgtgaaacg
2221   tttagcgatt gatagttgta ttgaatttgt tgcgcgagct gtcgctcaaa gtcattttaa
2281   agtattggaa ggtaatagaa ttcaaaagaa tgatgtttac tacaagttaa atataaaacc
2341   aaatactgac ttatcaagcg atagttttg gcaacaagtt atatataaac taatttatga
2401   taacgaggtt ttaatcgtag taagtgacag caaagaatta cttatcgcag atagctttta
2461   cagagaagag tacgctttgt atgatgatat attcaaagat gtaacggtta aagattatac
2521   ttatcaacgt actttcacaa tgcaagaggt catatattta aagtacaaca acaataaagt
2581   gacacacttt gtagaaagtc tattcgaaga ttacgggaaa atattcggaa gaatgatagg
2641   tgcacaatta aaaaactatc aaataagagg gattttgaaa tctgcctcta gcgcatatga
2701   cgaaaagaat atagaaaaat tacaagcgtt cacaaataaa ttattcaata ctttttaataa
```

Figure 2B

```
2761  aaatcaacta  gcaatcgcgc  ctttgataga  aggttttgat  tatgaggaat  tatctaatgg
2821  tggtaagaat  agtaacatgc  cttttctga   attgagtgag  ctaatgagag  atgcaataaa
2881  aaatgttgcg  ttgatgattg  gtatacctcc  aggtttgatt  tacggagaaa  cagctgattt
2941  ggaaaaaaac  acgcttgtat  ttgagaagtt  ctgtttaaca  cctttattaa  aaaagattca
3001  gaacgaatta  aacgcgaaac  tcataacaca  aagcatgtat  ttgaaagata  caagaataga
3061  aattgtcggt  gtgaataaaa  aagacccact  tcaatatgct  gaagcaattg  acaaacttgt
3121  aagttctggt  tcatttacaa  ggaatgaggt  gcggattatg  ttaggtgaag  aaccatcaga
3181  caatcctgaa  ttagacgaat  acctgattac  taaaaactac  gaaaaagcta  acagtggtga
3241  aaatgatgaa  aaagaaaaag  atgaaaacac  tttgaaaggt  ggtgatgaag  atgaaagcgg
3301  agattaaagg  cgtcatcgtt  tccaacgaag  ataaatgggt  ttacgaaatg  cttggtatgg
3361  attcgacttg  tcctaaagat  gttttaacac  aactagaatt  tagtgatgaa  gatgttgata
3421  ttataattaa  ctcaaatggt  ggtaacctag  tagctggtag  tgaaatatat  acacatttaa
3481  gagctcataa  aggcaaagtg  aatgttcgta  tcacagcaat  agcagcaagt  gcggcatcgc
3541  ttatcgcaat  ggctggtgac  cacatcgaaa  tgagtccggt  tgctagaatg  atgattcaca
3601  atccttcaag  tattgcgcaa  ggagaagtga  aagatctaaa  tcatgctgca  gaaacattag
3661  aacatgttgg  tcaaataatg  gctgaggcat  atgcggttag  agctggtaaa  aacaaacaag
3721  aacttataga  aatgatggct  aaggaaacgt  ggctaaatgc  tgatgaagcc  attgaacaag
3781  gttttgcgga  tagtaaaatg  tttgaaaacg  acaatatgca  aattgtagca  agcgatacac
3841  aagtgttatc  gaaagatgta  ttaaatcgtg  taacagcttt  ggtaagtaaa  acgccagagg
3901  ttaacattga  tattgacgca  atagcaaata  aagtaattga  aaaaataaat  atgaaagaaa
3961  aggaatcaga  aatcgatgtt  gcagatagta  aattatcagc  aaatggattt  tcaagattcc
4021  ttttttaata  caaaaatagg  aggtcataaa  atgactataa  atttatcgga  aacattcgca
4081  aatgcgaaaa  acgaatttat  taatgcagta  aacaacggtg  aaccgcaaga  aagacaaaat
4141  gaattgtacg  gtgacatgat  taaccaacta  tttgaagaaa  ctaaattaca  agcaaaagca
4201  gaagctgaaa  gagtttctag  tttacctaaa  tcagcacaaa  ctttgagtgc  aaaccaaaga
4261  aatttcttta  tggatatcaa  taagagtgtt  ggatataaag  aagaaaaact  tttaccagaa
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4381  ggtattaaaa  atgctggttt  gcgtttgaag  ttcttaaaat  ccgaaacttc  tggcgtggct
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4681  gtacaaaaag  gtgtatcggt  aactgatggt  gcttatccag  agaaagaaga  acaaggtacg
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5161  aaaccagctt  tagaagatac  cgaagaaaca  ctataaaatt  ttatgaggtg  ataaaatggt
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5641  aagaattgat  acttatacgc  gctagatatg  cttatcaaga  tttattagaa  cacttcaacg
5701  acaattacag  acctgaaata  atagattttt  cgttatctct  aatggaggta  tcagaagatg
```

Figure 2C

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5821 tataagtata ctgaaaataa tggtccagaa gctggagaaa aagaagaaaa attattatat
5881 agctgttggg cgagtattga tggtgtctgg ttacgtgaat tagaacaagc tatctcaaac
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6661 cgacgaccca atacctacaa cttatactga cggagatgag tgtgcatata gttatattgt
6721 ccaaatagat gtttttgtta agtacaatga tgaatataat gcgagaatca taagaaataa
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6961 tattaacatt actggtttag gtttcgctaa attaacgaaa gaaggcgcgg aattaaaata
7021 tagtgatatt acaaaaacaa gaggattaca aaaaattggt gttgaaactg gtggagaact
7081 aaaaacagct tatgctgatg gcggtccaat tgaatcaggg aatacagacg gagaaggtaa
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7441 tatctttgat tcagctaaca tgacaaatca tgatggagac ggtgaaaaag gcgaagaggc
7501 tttcttaaag aaaatttag gcgaagaata tactggaaac gtgacagagg gtaacgaaga
7561 aactttgtaa caaaaccggc ttcatcggaa actgcggtaa agtcggttaa tataccagat
7621 agcattaaaa cacttaaagt tggcgacaca tacgatttaa atgttgtagt agagccatct
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8341 tttcattatg tgctttccat atatcaaaat aaaaataatg acatttctga agaaaaagca
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8461 ttttagaaag gaggtaaaaa atgggagaaa gaataaaagg tttatctata ggtttggatt
8521 tagatgcagc aaatttaaat agatcatttg cagaaatcaa acgaaacttt aaaactttaa
8581 attctgactt aaaattaaca ggcaacaact tcaaatatac cgaaaaatca actgatagtt
8641 acaaacaaag gattaaagaa cttgatggaa ctatcacagg ttataagaaa aacgttgatg
8701 atttagccaa gcaatatgac aaggtatctc aagaacaggg cgaaaacagt gcagaagctc
```

Figure 2D

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 8761 aaaagttacg acaagaatat aacaaacaag caaatgagct gaattatttta gaaagagaat
 8821 tacaaaaaac atcagccgaa tttgaagagt tcaaaaaagc tcaagttgaa gctcaaagaa
 8881 tggcagaaag tggctgggga aaaaccagta aagttttga aagtatggga cctaaattaa
 8941 caaaaatggg tgatggttta aaatccattg gtaaaggttt gatgattggt gtaactgcac
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 9241 tgaaattcag tcatataaca ggttctgacg gtgtgcaagc cgtacagtta attacccgtg
 9301 caatgggcga tgcaggtatc gaagcaagtg aatatcaaag tgttttggat atggtagcaa
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 9481 gggaaaagtc aggcgttaat actgaaatag cattcagtgg tttgaaaaaa gctatatcaa
 9541 attggggtaa agctggtaaa aacccaagag aagaatttaa gaagacatta gcagaaattg
 9601 aaaagacgcc ggatatagct agcgcaacaa gtttagcgat tgaagcattt ggtgcaaagg
 9661 caggtcctga tttagcagac gctattaaag gtggtcgctt tagttatcaa gaatttttaa
 9721 aaactattga agattcccaa ggcacagtaa accaaacatt taaagattct gaaagtggct
 9781 ccgaaagatt taaagtagca atgaataaat taaaattagt aggtgctgat gtatgggctt
 9841 ctattgaaag tgcgtttgct cccgtaatgg aagaattaat caaaaagcta tctatagcgg
 9901 ttgattggtt ttccaattta agtgatggtt ctaaaagatc aattgttatt ttcagtggta
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10201 aatctgaaac atttagaaat tttgttaatg gtgcaattga aagtgttaaa caaacattta
10261 gtaattttat tcaatttatt caacctttcg ttgattctgt taaaaacatc tttaaacaag
10321 cgatatcagc aatagttgat ttcgcaaaag atatttggag tcaaatcaat ggattcttta
10381 atgaaaacgg aatttccatt gttcaagcac ttcaaaatat atgcaacttt attaaagcga
10441 tatttgaatt tattttaaat tttgtaatta aaccaattat gttcgcgatt tggcaagtga
10501 tgcaatttat ttggccggcg gttaaagcct tgattgtcag tacttgggag aacataaaag
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10681 aattaatttg gaatttagtt caattatggt ttgtaggtaa aatacttggt gttgttaggt
10741 actttggcgg gttgctaaaa ggattgatag caggaatttg ggacgtaata agaagtatat
10801 tcagtaaatc tttatcagca atttggaatg caacaaaaag tattttggga ttttttattta
10861 atagcgtaaa atcaattttc acaaatatga aaaattggtt atctaatact tggagcagta
10921 tccgtacgaa tacaatagga aaagcgcagt cattatttag tggcgtcaaa tcaaaattta
10981 ctaatttatg gaatgcgacg aaagaaattt ttagtaattt aagaaattgg atgtcaaata
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11101 gtggaatttt cacaaatatg cgcgatggct tgagttccat tatagataag attaaaagtc
11161 atatcggcgg tatggtaagc gctattaaaa aaggacttaa taaattaatc gacggtttaa
11221 actgggtcgg tggtaagttg ggaatggata aaatacctaa gttacacact ggtacagagc
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11341 cagttgggga taagggacgc ggaaatggtc caaatggttt tagaaatgaa atgattgaat
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11461 gctcaaaagt atacaacggt gcacaaactt attcaatgtt aaacggaacg cttccaagat
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11581 caaaagataa aataggtaaa ggtaccaaat ggcttggcga taaagttggc gatgtttttag
11641 attttatgga aaatccaggc aaactttttaa attatatact tgaagctttt ggaattgatt
11701 tcaattcttt aactaaaggt atgggaattg caggcgacat aacaaaagct gcatggtcta
```

Figure 2E

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11761 agattaagaa aagtgctact gattggataa aagaaaattt agaagctatg ggcggtggcg
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Figure 2F

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Figure 2G

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Figure 2H

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Figure 2I

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26521 caaaacttac ttttacaaca gcaagtagaa gttaacaaac caaaagtatt attcgctgac
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```

Figure 2J

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29641 ctgataacaa ttcagatatt agttactcca caaatagaaa tagagctagg gagtttaacg
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```

Figure 2K

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29881 tataaatttg cagtatacgg aaaaattggc tcaggaaaaa ccacgtttgc tacaagagat
29941 aaagacgctt tcgtcattga cattaacgaa ggtggaacaa cggttactga cgaaggatca
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Figure 2L

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Figure 2M

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Figure 2N

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39421 agcgcagata tacaagctag gttaaaagta ggcgataagg tagaagttaa aacaatcggt
39481 tatagaatac acttttaaa tttatatccg gtcttatacg aagtaaagaa ggtagataaa
39541 caatgattaa acaaatacta agactattat tcttactagc aatgtatgag ttaggtaagt
39601 atgtaactga gcaagtgtat attatgatga cggctaatga tgatgtagag gcgccgagtg
39661 attacgtctt tcgagcggag gtgagtgaat aatgagaata tttatttatg atttgatcgt
39721 tttgctgttt gctttcttaa tatccatata tattattgat gatggagtga taataaatgc
39781 attaggaatt tttggtatgt ataaaattat agattccttt tcagaaaata ttataaagag
39841 gtagataaaa atgaacgagc aaataatagg aagcatatat actttagcag gaggtgttgt
39901 gctttattca gttaaagaga ttttttaggta ttttacagat tctaacttac aacgtaaaaa
39961 aatcaattta gaacaaatat atccgatata tttagattgt tttaaaaagg ctaaaaagat
40021 gattggagct tatattattc caacagaaca gcatgaattt ttagatttt ttgatattga
40081 agtctttaat aatttagata agcaaagtaa aaaagcgtat gaaaatgtta ttggatttag
40141 acaaatgatt aatttatcaa atagagttaa ggcaatggaa gatttaaga tgagtttcaa
40201 caatgaattt agtacaaatc agattttttt taatccttct tttgttatgg aaacaattgc
40261 tattataaat gaatatcaaa aagatatatc ttatttaaaa aatataatta ataaaatgaa
40321 tgaaaataga gcttataatc atattgatag ttttatcact tcagagtacc gacgaaaat
40381 aaacgattat aatctttatc ttgataaatt tgaagaacag tttagtcaaa agtttaaaat
40441 aaacagaact tcgataaaag aaagaattat tattaattta aacaagagga gatttaaatg
40501 atgtggatta ctatgactat tgtatttgct atattgctat tagtttgtat cagtattaat
40561 agtgatcgtg caagagagat acaagcactt agatatatga atgattatct acttgatgaa
40621 gtagttaaaa ctaaagggta caacgggtta gaagaataca ggattgaatt gaagcgaatg
40681 aataacgata ttaaaaagta atttatatta tcggaggtat tgcattgaat gataaagatt
40741 gagaaacacg atatcaaaaa gcttgaagaa tacattcagc acatcgataa ctatcgaaga
40801 gagttgaaga tgcgagaata tgaattactt gaaagtcatg aaccagataa tgcgggagct
40861 ggcaaaagta atttgccggg taacccgatt gaacgatgtg caataaagaa gtttagtgat
40921 aacaggtaca atacattaag aaatatagtt aacggtgtag atagattgat aggtgaaagt
40981 gatgaggata cgcttgagtt attaaggttt agatattggg attgtcctat tggttgttat
41041 gaatgggaag atatagcaca ttactttggt acaagtaaga caagtatatt acgtagaagg
41101 aatgcactga tcgataagtt agcaaagtat attggttatg tgtagcggac ttttacccta
41161 tgtaagtccg cattaaaaca gtttattatg ttagtatcag attaatattt aaagttatta
41221 aatgctaata cgacgcatga acaagaggcg catcactatg tgatgtgtct ttttatttat
41281 gaggtatgaa catgttcaaa ctaattgtaa atacattact acacatcaag tatagatgag
41341 tcttgatact acttaagtta tataaggtga aacattatga tgactaaaga cgaacgtata
41401 cgattctata agtctaaaga atggcaaata acaagaaaaa gagtgctaga aagagataat
41461 tatgaatgtc aacaatgtaa gagagacggc aagttaacga catatgacaa aagcaagcgt
41521 aagtcgttgg atgtagatca tatattatcg ctagaacatc atccggagtt tgctcatgac
41581 ttaaacaatt tagaaacact gtgtattaaa tgtcacaaca aaaaagaaaa gagatttata
41641 aaaaaagaaa ataaatggaa agacgaaaaa tggtaaatac ccccgggtca aaaaaatcaa
41701 aagcgatc
```

Fig. 3

Phage: Bacteriophage 77
Minimal ORF size: 33 a.a.
ORFs "with" RBS.
Number of ORFs: 99

037: Bacteriocin precursor;
003: Terminase; Inhibitor;
015: ATP-dependent CLP protease.
001: Capsid; Inhibitor;

084: Staph;
096: Staph;
082: Structural;

075: Staph;

035: Holin;
005: Amidase; Staph;
007: Integrase; Staph;
011: DNA repair repressor;
077: Staph;
046: Staph;

065: Staph;
014: Anti-repressor;
012: Staph;
022: Staph;
018: Staph; Mito. energy transfer signature;
010: Antirepressor; DNA-binding; Staph;
102: Staph; Inhibitor;
079: Staph;
182: Staph; Inhibitor;
043: Staph; Inhibitor;

104: Inhibitor; Staph;
038: Staph;   112: RinB; Staph;
028: Staph;   040: Cytochrome c signature;
088: Staph;
175: Staph;

030: Staph;
050: Staph;
036: Staph;
021: dUTPase;
049: Staph;
120: Staph;
070: Staph;
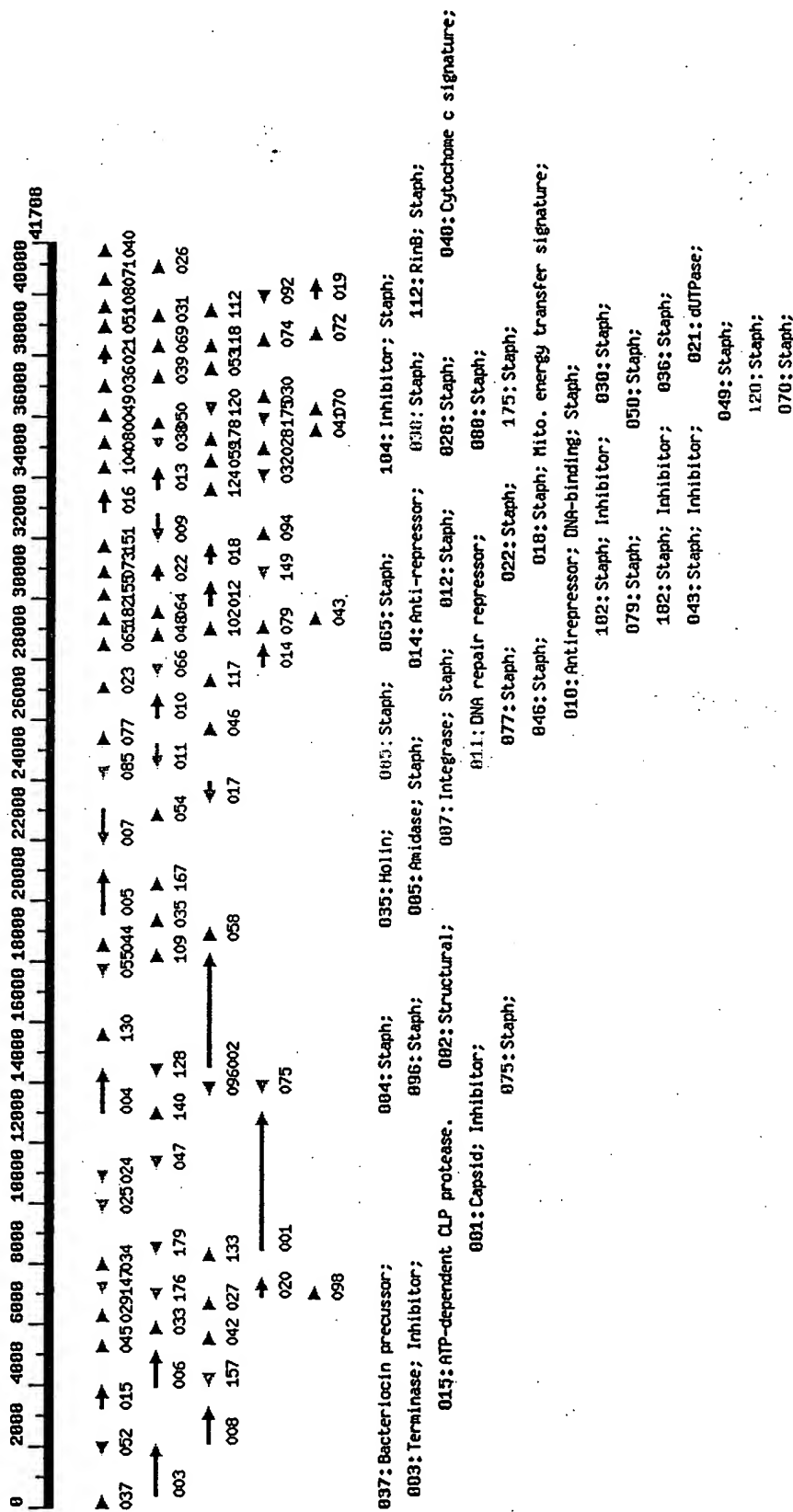
Fig. 4

P77ORF104

SEQ ID NO: 4

1   atggtaacca aagaattttt aaaaactaaa cttgagtgtt cagatatgta cgctcagaaa
61   ctcatagatg aggcacaggg cgatgaaaat aggttgtacg acctatttat ccaaaaactt
121   gcagaacgtc atacacgccc cgctatcgtc gaatattaa

SEQ ID NO: 5

1   MVTKEFLKTK LECSDMYAQK LIDEAQGDEN RLYDLFIQKL AERHTRPAIV EY

Fig. 5

Predicted Tryptic Peptide Masses of Conceptual ORF in Contig 1383:

```
  1   M G G G Q S I M K q f k S I I N T S Q D F E K r I E K i k K   30
 31   e v i n d p d v k Q F L E A H R a e l t n a m i d e d l n v   60
 61   l q e y k D Q Q K h y d g h k F A D C P N F V K g h v p e l   90
 91   y v d n n r I K i r Y L Q C P C K i k Y D E E R i e a e l i   120
121   t s n n m q r D T L N A K l k D I Y M N H R d r L D V A M A   150
151   A D D I C T A I T N G E Q V K g l y l y g p f g t g k S F I   180
181   L G A I A N Q L K s k K v r S T I I Y L P E F I R t l k G G   210
211   F K d g s f e k K I h r V R e a n i l m l a a i g a e e v t   240
241   p w v r D E V I G P L L H Y R m v h e l p t f f s s n f d y   270
271   s e l e h h l a m t r D G E E K t k A A R i i e r V K s l s   300
301   t p y f l s g e n f r N N                                    313
```

Tryptic peptide fragment:

GHVPELYVDNNR   Predicted Peptide Mass MH+ = 1413.538

STIIYLPEFIR   Predicted Peptide Mass MH+ = 1352.6221

SLSTPYFLSGENFR   Predicted Peptide Mass MH+ = 1618.7923

Figure 6A

SEQ ID NO: 6   DnaC nucleotide *B. subtillis*

```
   1   ATGACAGACC TTCTGAATGA CCGGCTTCCT CCGCAAAATA TAGAAGCCGA
  51   ACAAGCCGTG TTAGGCGCTA TTTTTTTACA GCCGTCTGCT TTAACACTGG
 101   CTTCAGAAGT ATTGATTCCA GATGATTTCT ATAGAATGTC CCACCAAAAA
 151   ATCTATAATG CGATGCTGGT GCTCGGTGAC CGAGGTGAAC CGGTTGATCT
 201   GGTGACAGTT ACATCAGAGC TTGCGAACAC AGACCTGCTG GAAGAAGTAG
 251   GCGGTATTTC ATATTTGACA GATATCGCAA ACTCGGTGCC GACAGCGGCT
 301   AACATAGAAT ATTACGCGAA AATCGTTGAG GAAAAATCGA TTCTTCGCCG
 351   ATTAATCAGA ACTGCGACAA CGATTGCTCA AGACGGGTAT ACCCGTGAGG
 401   ATGAGGTCGA GGATTTACTC AGTGAAGCGG AAAAAACGAT TATGGAAGTG
 451   GCACAGCGCA AAAACACGAG TGCCTTCCAA AATATTAAGG ACGTCCTTGT
 501   CCAGACCTAT GATAATATCG AACAGCTTTA CAATCGAAAA GGTGATATCA
 551   CGGGAATTCC AACAGGGTTT ACGGAGCTTG ACCGGATGAC TGCGGGTTTC
 601   CAGCGCAACG ACTTGATCAT TGTGGCTGCC CGTCCTTCAG TAGGGAAAAC
 651   AGCCTTTGCC CTGAACATCG CACAAAACGT GGCGACGAAG ACCGATGAGA
 701   GCGTAGCGAT TTTCAGTCTT GAGATGGGTG CCGAGCAGCT CGTTATGCGT
 751   ATGCTCTGTG CCGAGGGAAA TATCAATGCC CAGAATCTCC GTACAGGTAA
 801   CCTGACCGAA GAGGATTGGG GCAAGCTGAC GATGGCAATG GGAAGCCTAT
 851   CGAACAGCGG GATTTACATC GATGATACAC CGGGTATTCG AGTGAGTGAA
 901   ATCCGTGCCA AGTGCCGCCG CTTGAAGCAG GAAAGCGGGC TGGGCATGAT
 951   TTTGATCGAT TACCTGCAAT TGATTCAGGG AAGCGGTCGT TCAAAGGACA
1001   ACCGTCAGCA GGAAGTATCT GAAATTTCCC GTGAACTGAA GTCGATTGCG
1051   AGGGAGCTGC AAGTCCCTGT TATCGCGCTT TCTCAGCTTT CCAGGGGTGT
1101   TGAGCAGCGT CAGGATAAAC GTCCGATGAT GTCTGATATC CGGGAATCAG
1151   GAAGTATCGA GCAGGACGCG GATATTGTCG CGTTCCTTTA TCGTGATGAC
1201   TACTATGACA AAGAAACCGA GAATAAAAAT ATTATCGAAA TTATTATCGC
1251   CAAACAGCGT AACGGCCCGG TAGGAACCGT GTCTCTTGCG TTCGTAAAAG
1301   AATACAACAA ATTCGTCAAC CTGGAACGGC GTTTTGATGA CGCAGGCGTT
1351 CCGCCCGGCG CA
```

Figure 6B

SEQ ID NO: 7   DnaC nucleotide *S. aureus*

```
   1  ATGGATAGAA TGTATGAGCA AAATCAAATG CCGCATAACA ATGAAGCTGA
  51  ACAGTCTGTC TTAGGTTCAA TTATTATAGA TCCAGAATTG ATTAATACTA
 101  CTCAGGAAGT TTTGCTTCCT GAGTCGTTTT ATAGGGGTGC CCATCAACAT
 151  ATTTTCCGTG CAATGATGCA CTTAAATGAA GATAATAAAG AAATTGATGT
 201  TGTAACATTG ATGGATCAAT TATCGACGGA AGGTACGTTG AATGAAGCGG
 251  GTGGCCCGCA ATATCTTGCA GAGTTATCTA CAAATGTACC AACGACGCGA
 301  AATGTTCAGT ATTATACTGA TATCGTTTCT AAGCATGCAT TAAAACGTAG
 351  ATTGATTCAA ACTGCAGATA GTATTGCCAA TGATGGATAT AATGATGAAC
 401  TTGAACTAGA TGCGATTTTA AGTGATGCAG AACGTCGAAT TTTAGAGCTA
 451  TCATCTTCTC GTGAAAGCGA TGGCTTTAAA GACATTCGAG ACGTCTTAGG
 501  ACAAGTGTAT GAAACAGCTG AAGAGCTTGA TCAAAATAGT GGTCAAACAC
 551  CAGGTATACC TACAGGATAT CGAGATTTAG ACCAAATGAC AGCAGGGTTC
 601  AACCGAAATG ATTTAATTAT CCTTGCAGCG CGTCCATCTG TAGGTAAGAC
 651  TGCGTTCGCA CTTAATATTG CACAAAAAGT TGCAACGCAT GAAGATATGT
 701  ATACAGTTGG TATTTTCTCG CTAGAGATGG GTGCTGATCA GTTAGCCACA
 751  CGTATGATTT GTAGTTCTGG AAATGTTGAC TCAAACCGCT TAAGAACGGG
 801  TACTATGACT GAGGAAGATT GGAGTCGTTT TACTATAGCG GTAGGTAAAT
 851  TATCACGTAC GAAGATTTTT ATTGATGATA CACCGGGTAT TCGAATTAAT
 901  GATTTACGTT CTAAATGTCG TCGATTAAAG CAAGAACATG GCTTAGACAT
 951  GATTGTGATT GACTACTTAC AGTTGATTCA AGGTAGTGGT TCACGTGCGT
1001  CCGATAACAG ACAACAGGAA GTTTCTGAAA TCTCTCGTAC ATTAAAAGCA
1051  TTAGCCCGTG AATTAGAATG TCCAGTTATC GCATTAAGTC AGTTATCTCG
1101  TGGTGTTGAA CAACGACAAG ATAAACGTCC AATGATGAGT GATATTCGTG
1151  AATCTGGTTC GATTGAGCAA GATGCCGATA TCGTTGCATT CTTATACCGT
1201  GATGATTACT ATAACCGTGG CGGCGATGAA GATGATGACG ATGATGGTGG
1251  TTTCGAGCCA CAAACGAATG ATGAAACGG TGAAATTGAA ATTATCATTG
1301  CTAAGCAACG TAACGGTCCA ACAGGCACAG TTAAGTTACA TTTTATGAAA
1351  CAATATAATA AATTTACCGA TATCGATTAT GCACATGCAG ATATGATGTA
1401  A
```

Figure 6C

Optimal global alignment
Sequence 1 SEQ ID NO: 6   DnaC nucleotide *B. subtillis*(1471 letters)
Sequence 2 SEQ ID NO: 7   DnaC nucleotide *S. aureus*(1513 letters)

```
seq1    1 AT-GACAGACCTTCTGAATGACCGGCTTC---CTCCGCAAAATATAGAAGCCGAACAAGC    56
          || || |||     || ||||| |     ||     ||||| || | ||||| ||||| |
seq2    1 ATGGATAGA----ATGTATGAGCAAAATCAAATGCCGCATAACAATGAAGCTGAACAGTC    56

seq1   57 CGTGTTAGGCGCTATTTTTTTACAGCC-GTCTGCTTTAACACTGGCTTCAGAAGTATTGA   115
          || ||||||  | ||| || || | || |   | |||| ||| ||  | ||||| |||
seq2   57 TGTCTTAGGTTCAATTATTATAGATCCAGAATTGATTAATACT-ACTCAGGAAGTTTTGC   115

seq1  116 TTCCAGATGATTTCTATAGAATGTCCCACCAAAAAATCTATAATGCGATGCTGGTGCTCG   175
          |||| ||   || |||||    |||| ||| | ||| | |   ||| ||| || ||   |
seq2  116 TTCCTGAGTCGTTTTATAGGGGTGCCCATCAACATATTTTCCGTGCAATGATGCACTTAA   175

seq1  176 GTGACCGAGGTGAACCGGTTGATCTGGTGACA--GTTACATCAGAGCTTGCGAACACAGA   233
          |||     | ||   ||||| | ||| |  | |   ||| | | ||    ||
seq2  176 ATGAAGATAATAAAGAAATTGATGTTGTAACATTGATGGATC--AATTATCGACGGAAGG   233

seq1  234 CCTGCTGGAAGAAGTAGGCGGTATTTCATAT-TTG-ACAGATATCGCAAACTCGGTGCCG   291
           | || | |||| || ||    |||| ||| ||| | | |||| ||  || | || |
seq2  234 TACGTTGAATGAAGCGGGTGGCCCGCAATATCTTGCAGAGTTATCTACAAAT--GTACCA   291

seq1  292 ACAGCGGCTAACATAGAATATTACGCGAAAATCGTTGAGGAAAAATCGATT-CTTCGCCG   350
          ||  ||  ||     | |  |||||| |   | ||||||    || || ||| || |
seq2  292 ACGACGCGAAATGTTCAGTATTATACTGATATCGTT-TCTAAGCATGCATTAAAACGTAG   350

seq1  351 ATTAATCAGAACTGCGACAACGATTGCTCAAGACGGGTATACCCGTGAGGATGAGGTCGA   410
          ||| ||  ||||||   | |||||  | || || |||   ||| || | ||| || | ||
seq2  351 ATTGATTCAAACTGCAGATAGTATTGCCAATGATGGATATAATGATGAACTTGAACTAGA   410

seq1  411 --GGATTTACTCAGTGAAGCGGAAAAAACGATTATGGAAGTGGCA-CAGCGCAAAAACAC   467
            ||||| | ||||| || |||    ||| | ||| | ||| | || | |  || |
seq2  411 TGCGATTT--TAAGTGATGCAGAACGTCGAATTTTAGAGCTATCATCTTCTCGTGAAAGC   468

seq1  468 GAGTGCCTTCCAAAATATTAAGGACGTCCTTGTCCAGACCTATGATAATATC-GAACAGC   526
          || || |||  || | |||     |||||| | |  || ||||| || | | ||| |||
seq2  469 GA-TGGCTTTAAAGACATTCGAGACGTCTTAGGACAAGTGTATGA-AACAGCTGAAGAGC   526

seq1  527 TTTACAATCGAAAAGGTGAT--ATCA-CGGGAATTCCAACAGGGTTTACGGAGCTTGACC   583
          ||     ||| |||  ||| |  | | || || || || ||||||| | |  || | ||||
seq2  527 TT---GATCAAAATAGTGGTCAAACACCAGGTATACCTACAGGATATCGAGATTTAGACC   583

seq1  584 GGATGACTGCGGGTTTCCAGCGCAACGACTTGATCATTGTGGCTGCCCGTCCTTCAGTAG   643
          |||||  || || ||| | || || || || || || || | || || | || |||||| || ||||
seq2  584 AAATGACAGCAGGGGTTCAACCGAAATGATTTAATTATCCTTGCAGCGCGTCCATCTGTAG   643

seq1  644 GGAAAACAGCCTTTGCCCTGAACATCGCACAAAACGTGGCGAC----GAAGACCGATG-A   698
          | || || || || || || || || || || ||||||||| || || || |||||  ||| |
seq2  644 GTAAGACTGCGTTCGCACTTAATATTGCACAAAAAGTTGCAACGCATGAAGA--TATGTA   701
```

Figure 6C Cont.

```
seq1    699 GAGCGTAGCGATTTTCAGTCTTGAGATGGGTGCCGAGCAGCTCGTTATGCGTATGCTCTG    758
            |  || |   |||||||   || |||||||||||| || ||| | |   | |||||| | ||
seq2    702 TACAGTTGGTATTTTCTCGCTAGAGATGGGTGCTGATCAGTTAGCCACACGTATGATTTG    761

seq1    759 TGCCGAGGGAAATATCAATGCCCAGAATC---TCCGTACAGGTAACCTGACCGAAGAGGA    815
            |    ||||||  |   || |  || |    | |  ||  |||| |||| || || ||
seq2    762 TAGTTCTGGAAATGT---TGACTCAAACCGCTTAAGAACGGGTACTATGACTGAGGAAGA    818

seq1    816 TTGGGGCAAGCTGACGATGGCAATGGGAAGCCTATCGAACAGCGGGATTTACATCGATGA    875
            |||| |     | || || || | ||| |    |||| |      ||||| || |||||
seq2    819 TTGGAGTCGTTTTACTATAGCGGTAGGTAAATTATCACGTACGAAGATTTTTATTGATGA    878

seq1    876 TACACCGGGTATTCGAGTGAGTGAAATCCGTGCCAAGTGCCGCCGCTTGAAGCAGGAAAG    935
            ||||||||||||||| | | ||| | ||| | || || || || || || ||||| |||
seq2    879 TACACCGGGTATTCGAATTAATGATTTACGTTCTAAATGTCGTCGATTAAAGCAAGAACA    938

seq1    936 CGGGCTGGGCATGATTTTGATCGATTACCTGCAATTGATTCAGGGAAGCGGT---CGTTC    992
            ||  |  | ||||||||| |||| || ||| | || |||||||||| || || |||  |  
seq2    939 TGGCTTAGACATGATTGTGATTGACTACTTACAGTTGATTCAAGGTAGTGGTTCACGTGC    998

seq1    993 AAAGGACAACCGTCAGCAGGAAGTATCTGAAATTTCCCGTGAACTGAAGTCGATTGCGAG   1052
            ||  ||| | || ||||||||||| ||||||||| || |||  | | ||  |  | || |
seq2    999 GTCCGATAACAGACAACAGGAAGTTTCTGAAATCTCTCGTACATTAAAAGCATTAGCCCG   1058

seq1   1053 GGAGCTGCAAGTCCCTGTTATCGCGCTTTCTCAGCTTTCCAGGGGTGTTGAGCAGCGTCA   1112
            ||  |   ||  || ||||||||  || |   |||| ||| | |||||||| || || ||
seq2   1059 TGAATTAGAATGTCCAGTTATCGCATTAAGTCAGTTATCTCGTGGTGTTGAACAACGACA   1118

seq1   1113 GGATAAACGTCCGATGATGTCTGATATCCGGGAATCAGGAAGTATCGAGCAGGACGCGGA   1172
            ||||||||||| |||||| |||| ||||||| || |||||| ||   || |||||| || ||
seq2   1119 AGATAAACGTCCAATGATGAGTGATATTCGTGAATCTGGTTCGATTGAGCAAGATGCCGA   1178

seq1   1173 TATTGTCGCGTTCCTTTATCGTGATGACTACT----------------------ATGA   1208
            ||| || || ||| | || |||||||| ||||                        ||||
seq2   1179 TATCGTTGCATTCTTATACCGTGATGATTACTATAACCGTGGCGGCGATGAAGATGATGA   1238

seq1   1209 CAAAGA----------------AACCGA--GAATAAAA--ATATTATCGAAATTATTAT   1247
            | | ||                || |||  || ||||   | || |||||||||| ||
seq2   1239 CGATGATGGTGGTTTCGAGCCACAAACGAATGATGAAAACGGTGAAATTGAAATTATCAT   1298

seq1   1248 CGCCAAACAGCGTAACGGCCCGGTAGGAACCGTGTCTCTTGC-GTTCGTAAAAGAATACA   1306
            || || || |||||||| ||    ||| || || || |    || | | ||  ||| |||| |
seq2   1299 TGCTAAGCAACGTAACGGTCCAACAGGCACAGT-TAAGTTACATTTTATGAAACAATATA   1357

seq1   1307 ACAAATTCGTCAACCTGGAACGGCGTTTTGATGACGCAGGCGTTCCGCCCGGCGCA   1362
            | |||||        |||    | ||     || ||    | |||| |     |
seq2   1358 ATAAATT----TACCGATATCG--ATTATGCACATGCAGATATGATG------TAA   1401
```

Figure 6D

SEQ ID NO: 8   DnaC *B. subtilis*

```
  1    MTDLLNDRLP  PQNIEAEQAV  LGAIFLQPSA  LTLASEVLIP  DDFYRMSHQK
 51    IYNAMLVLGD  RGEPVDLVTV  TSELANTDLL  EEVGGISYLT  DIANSVPTAA
101    NIEYYAKIVE  EKSILRRLIR  TATTIAQDGY  TREDEVEDLL  SEAEKTIMEV
151    AQRKNTSAFQ  NIKDVLVQTY  DNIEQLYNRK  GDITGIPTGF  TELDRMTAGF
201    QRNDLIIVAA  RPSVGKTAFA  LNIAQNVATK  TDESVAIFSL  EMGAEQLVMR
251    MLCAEGNINA  QNLRTGNLTE  EDWGKLTMAM  GSLSNSGIYI  DDTPGIRVSE
301    IRAKCRRLKQ  ESGLGMILID  YLQLIQGSGR  SKDNRQQEVS  EISRELKSIA
351    RELQVPVIAL  SQLSRGVEQR  QDKRPMMSDI  RESGSIEQDA  DIVAFLYRDD
401    YYDKETENKN  IIEIIIAKQR  NGPVGTVSLA  FVKEYNKFVN  LERRFDDAGV
451    PPGA
```

SEQ ID NO: 9   DnaC *S. aureus*

```
  1    MDRMYEQNQM  PHNNEAEQSV  LGSIIIDPEL  INTTQEVLLP  ESFYRGAHQH
 51    IFRAMMHLNE  DNKEIDVVTL  MDQLSTEGTL  NEAGGPQYLA  ELSTNVPTTR
101    NVQYYTDIVS  KHALKRRLIQ  TADSIANDGY  NDELELDAIL  SDAERRILEL
151    SSSRESDGFK  DIRDVLGQVY  ETAEELDQNS  GQTPGIPTGY  RDLDQMTAGF
201    NRNDLIILAA  RPSVGKTAFA  LNIAQKVATH  EDMYTVGIFS  LEMGADQLAT
251    RMICSSGNVD  SNRLRTGTMT  EEDWSRFTIA  VGKLSRTKIF  IDDTPGIRIN
301    DLRSKCRRLK  QEHGLDMIVI  DYLQLIQGSG  SRASDNRQQE  VSEISRTLKA
351    LARELECPVI  ALSQLSRGVE  QRQDKRPMMS  DIRESGSIEQ  DADIVAFLYR
401    DDYYNRGGDE  DDDDDGGFEP  QTNDENGEIE  IIIAKQRNGP  TGTVKLHFMK
451    QYNKFTDIDY  AHADMM
```
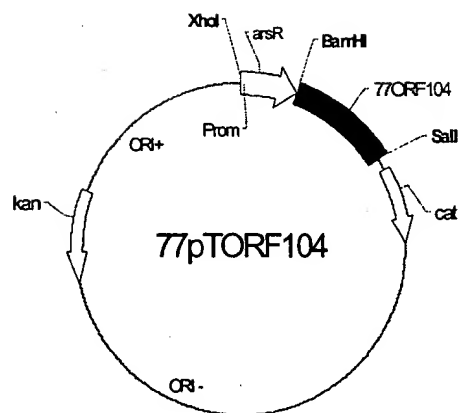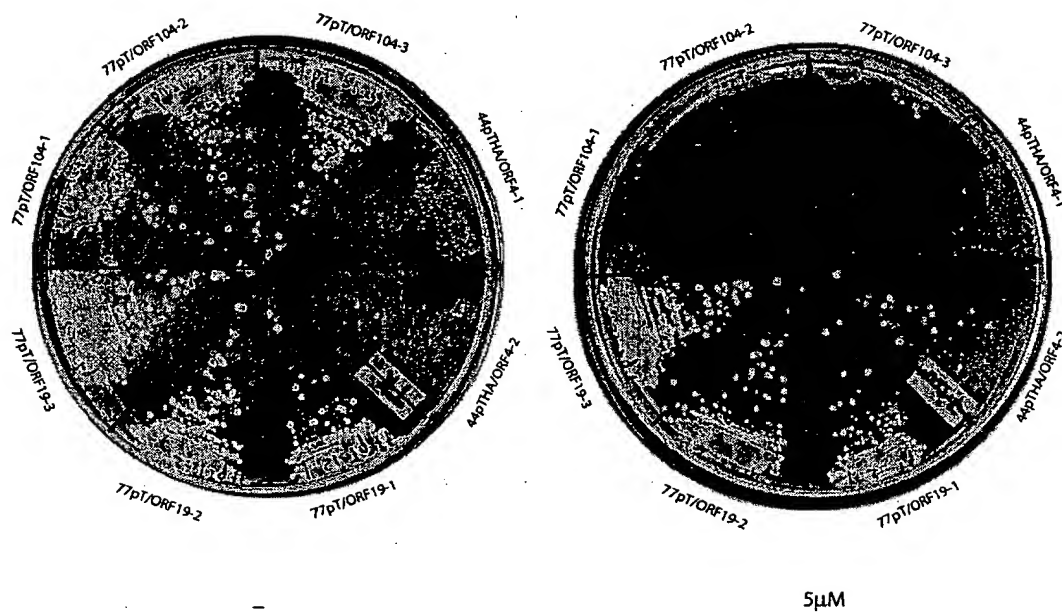
Figure 6E

Sequence 1 SEQ ID NO: 8 DnaC *B. subtilis*(490 letters)
Sequence 2 SEQ ID NO: 9 DnaC *S. aureus* (503 letters)

```
seq1     1 MTDLLNDRLPPQNIEAEQAVLGAIFLQPSALTLASEVLIPDDFYRMSHQKIYNAMLVLGD    60
           | :        | | ||||:|||:| : |   :    |||:|: ||| :|| |: ||: | :
seq2     1 MDRMYEQNQMPHNNEAEQSVLGSIIIDPELINTTQEVLLPESFYRGAHQHIFRAMMHLNE    60

seq1    61 RGEPVDLVTVTSELANTDLLEEVGGISYLTDIANSVPTAANIEYYAKIVEEKSILRRLIR   120
           : :|:||: :|:    | | ||  || ::: :|||  |:::||  || : :: ||||:
seq2    61 DNKEIDVVTLMDQLSTEGTLNEAGGPQYLAELSTNVPTTRNVQYYTDIVSKHALKRRLIQ   120

seq1   121 TATTIAQDGYTREDEVEDLLSEAEKTIMEVAQRKNTSAFQNIKDVLVQTYDNIEQLYNRK   180
           || :|| |||   | |:: :||:||: |:|:: : :  |:::|:||| | |: |:|
seq2   121 TADSIANDGYNDELELDAILSDAERRILELSSSRESDGFKDIRDVLGQVYETAEELDQNS   180

seq1   181 GDITGIPTGFTELDRMTAGFQRNDLIIVAARPSVGKTAFALNIAQNVATKTD-ESVAIFS   239
           |    |||||: :||:||||| ||||||:||||||||||||||||| ||| |   :| |||
seq2   181 GQTPGIPTGYRDLDQMTAGFNRNDLIILAARPSVGKTAFALNIAQKVATHEDMYTVGIFS   240

seq1   240 LEMGAEQLVMRMLCAEGNINAQNLRTGNLTEEDWGKLTMAMGSLSNSGIYIDDTPGIRVS   299
           |||||:|| ||:|: ||::: |||| :||||| : |:|:| || : |:|||||||||::
seq2   241 LEMGADQLATRMICSSGNVDSNRLRTGTMTEEDWSRFTIAVGKLSRTKIFIDDTPGIRIN   300

seq1   300 EIRAKCRRLKQESGLGMILIDYLQLIQGSG-RSKDNRQQEVSEISRELKSIARELQVPVI   358
           ::|:||||||||| || ||:||||||||| |: ||||||||||||||| ||::||||: |||
seq2   301 DLRSKCRRLKQEHGLDMIVIDYLQLIQGSGSRASDNRQQEVSEISRTLKALARELECPVI   360

seq1   359 ALSQLSRGVEQRQDKRPMMSDIRESGSIEQDADIVAFLYRDDYYDK--------------   404
           |||||||||||||||||||||||||||||||||||||||||||||:: 
seq2   361 ALSQLSRGVEQRQDKRPMMSDIRESGSIEQDADIVAFLYRDDYNRGGDEDDDDGGFEP    420

seq1   405 ETENKN-IIEIIIAKQRNGPVGTVSLAFVKEYNKFVNLERRFDDAGVPPGA           454
           :| ::| |||||||||||| ||| | |:|:||| :::      |
seq2   421 QTNDENGEIEIIIAKQRNGPTGTVKLHFMKQYNKFTDIDYAHADM-----M           466
```

FIGURE 7

7A-

XhoI | arsR | BamHI

Prom | 77ORF104

SalI

ORI+

kan

cat

77pTORF104

ORI-

7B-

77pT/ORF104-2 | 77pT/ORF104-3

77pT/ORF104-1 | 44pTHA/ORF4-1

77pT/ORF19-3 | 44pTHA/ORF4-2

77pT/ORF19-2 | 77pT/ORF19-1

—

77pT/ORF104-2 | 77pT/ORF104-3

77pT/ORF104-1 | 44pTHA/ORF4-1

77pT/ORF19-3 | 44pTHA/ORF4-2

77pT/ORF19-2 | 77pT/ORF19-1

5μM

7C-

Bacterial Growth kinetics

CFU X 10e6 / ml

1000

100

10

1

0   40   80   120   160   200   240

Time (min.)

- Non killer ORF, no induction
- Non killer ORF, induction
- 77pTORF104, no induction
- 77pTORF104, induction

GST   GST/ ORF104

ACB 0 0.1 0.5 1.0 2.0   ACB 0 0.1 0.5 1.0 2.0 Mr

Fig. 8 A

GST   GST/ ORF104

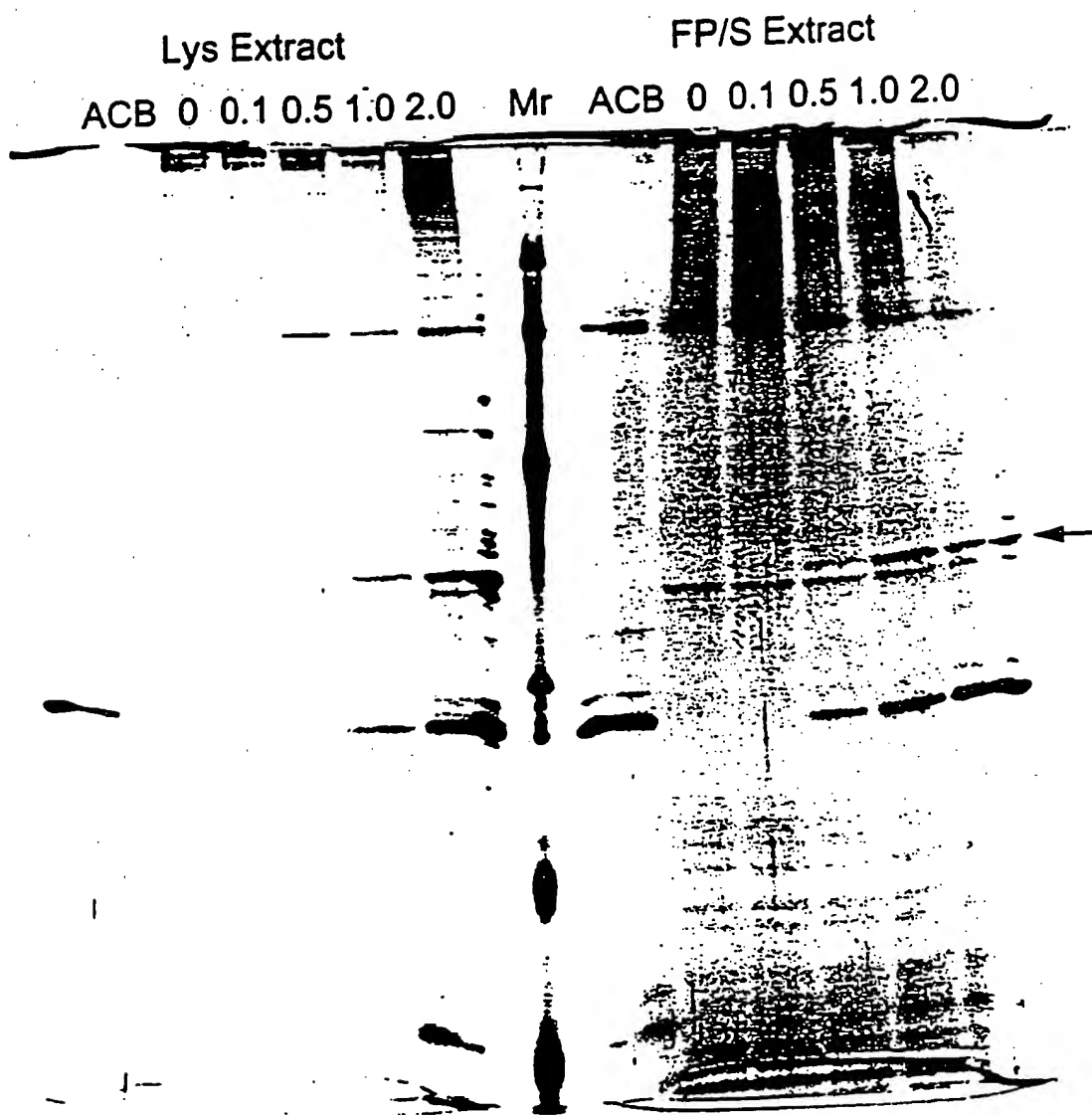ACB 0 0.1 0.5 1.0 2.0   Mr   ACB 0 0.1 0.5 1.0 2.0
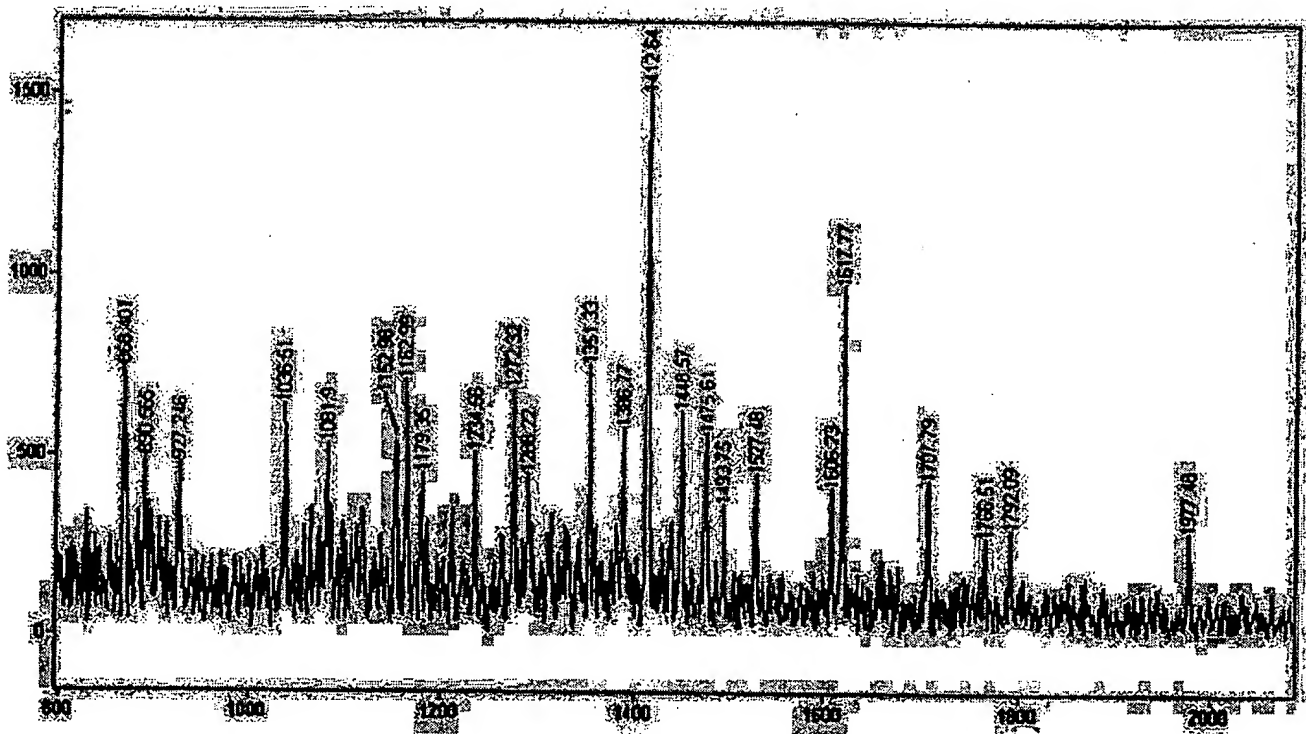
8B

GST   GST/ ORF104

Mr ACB 0 0.1 0.5 1.0 2.0   ACB 0 0.1 0.5 1.0 2.0

97

66

45

30

21

15

8C

GST   GST/ ORF104

Mr ACB 0 0.1 0.5 1.0 2.0 Mr ACB 0 0.1 0.5 1.0 2.0

97

66

45

30

21

15

8D

GST

GST/ ORF104   C   L

ACB 0 0.1 0.5 1.0 2.0   Mr   ACB 0 0.1 0.5 1.0 2.0   2.0 2.0

Fig. 9

Lys Extract   FP/S Extract

ACB 0 0.1 0.5 1.0 2.0   Mr   ACB 0 0.1 0.5 1.0 2.0
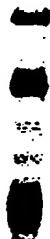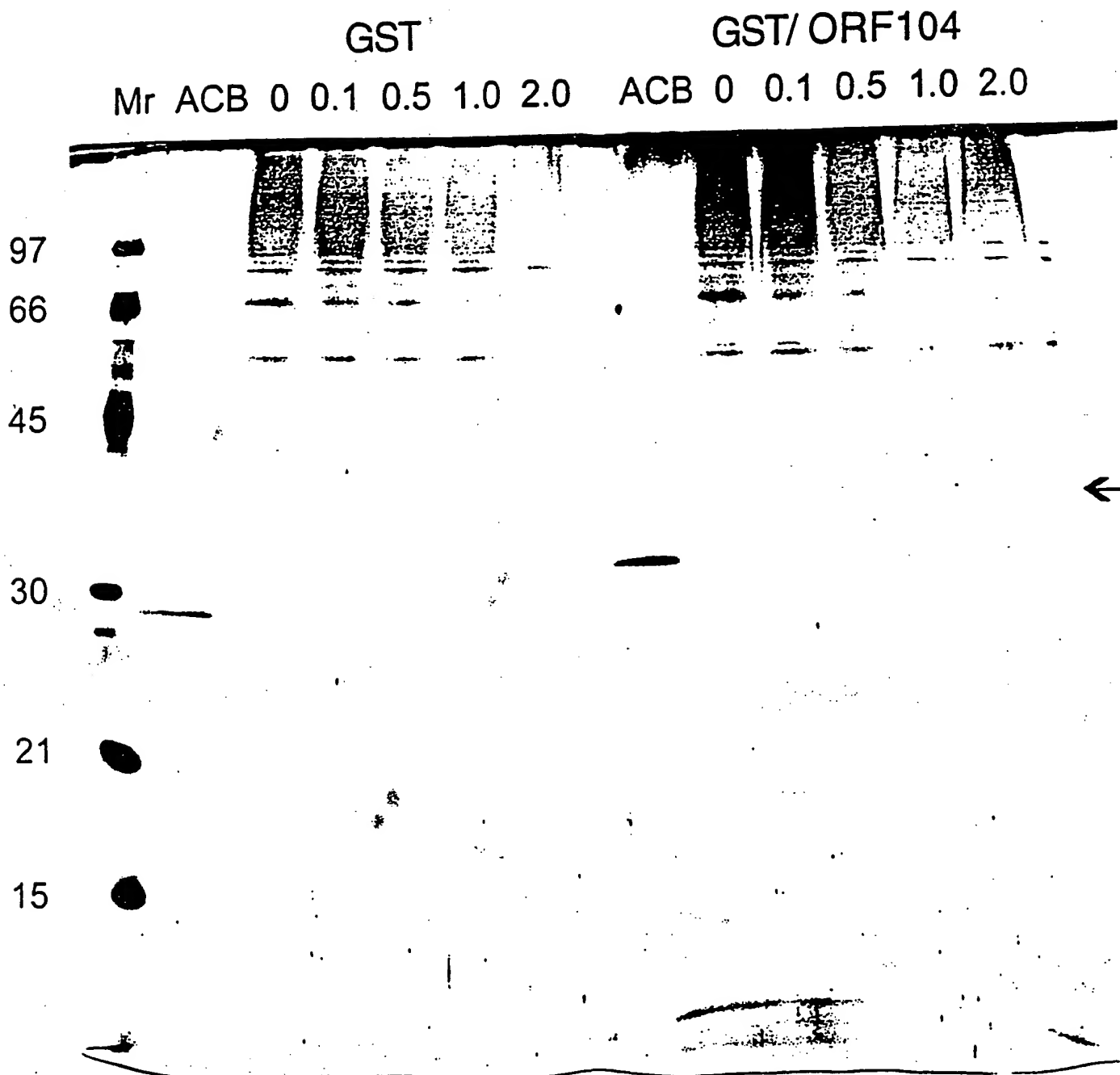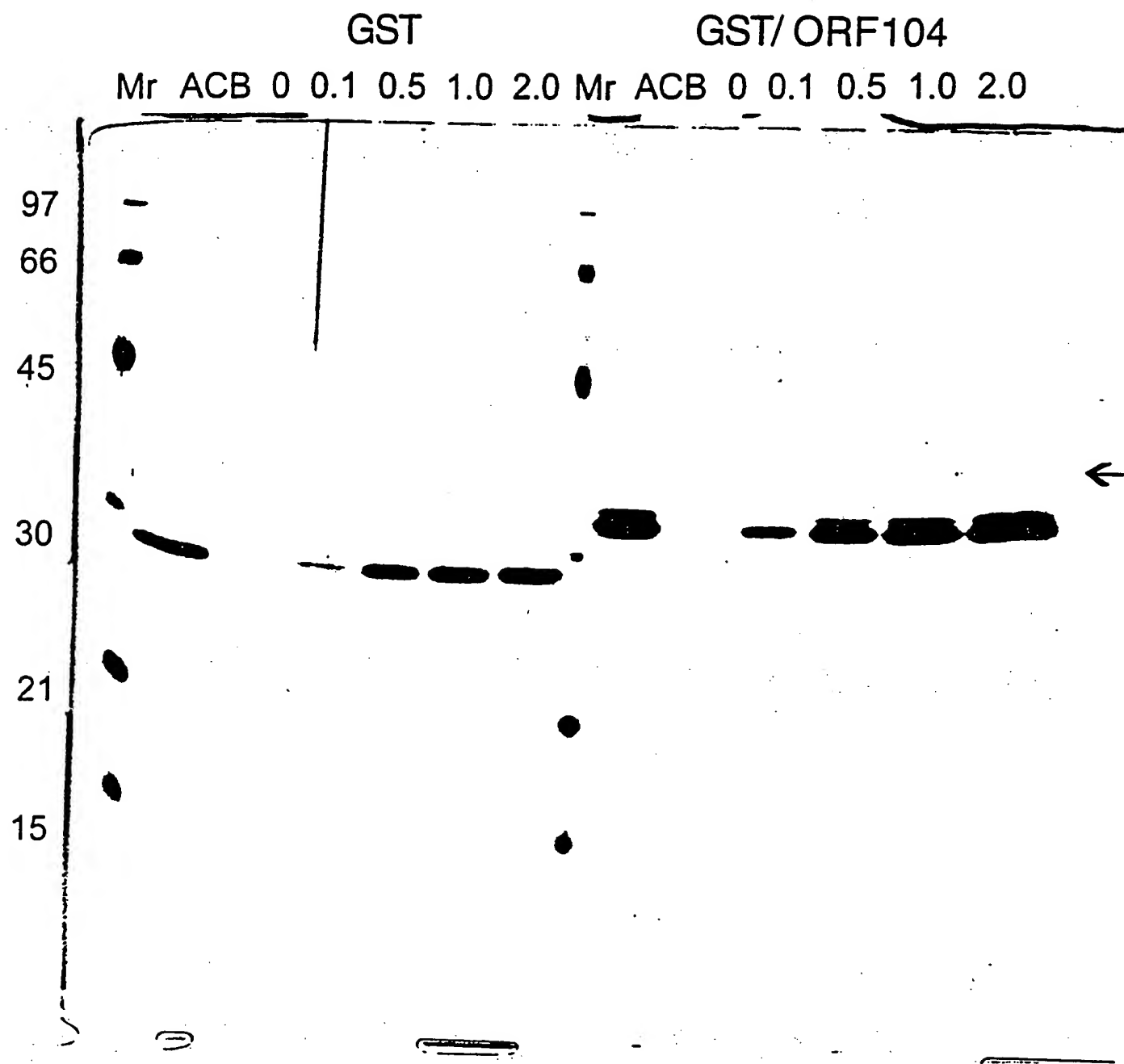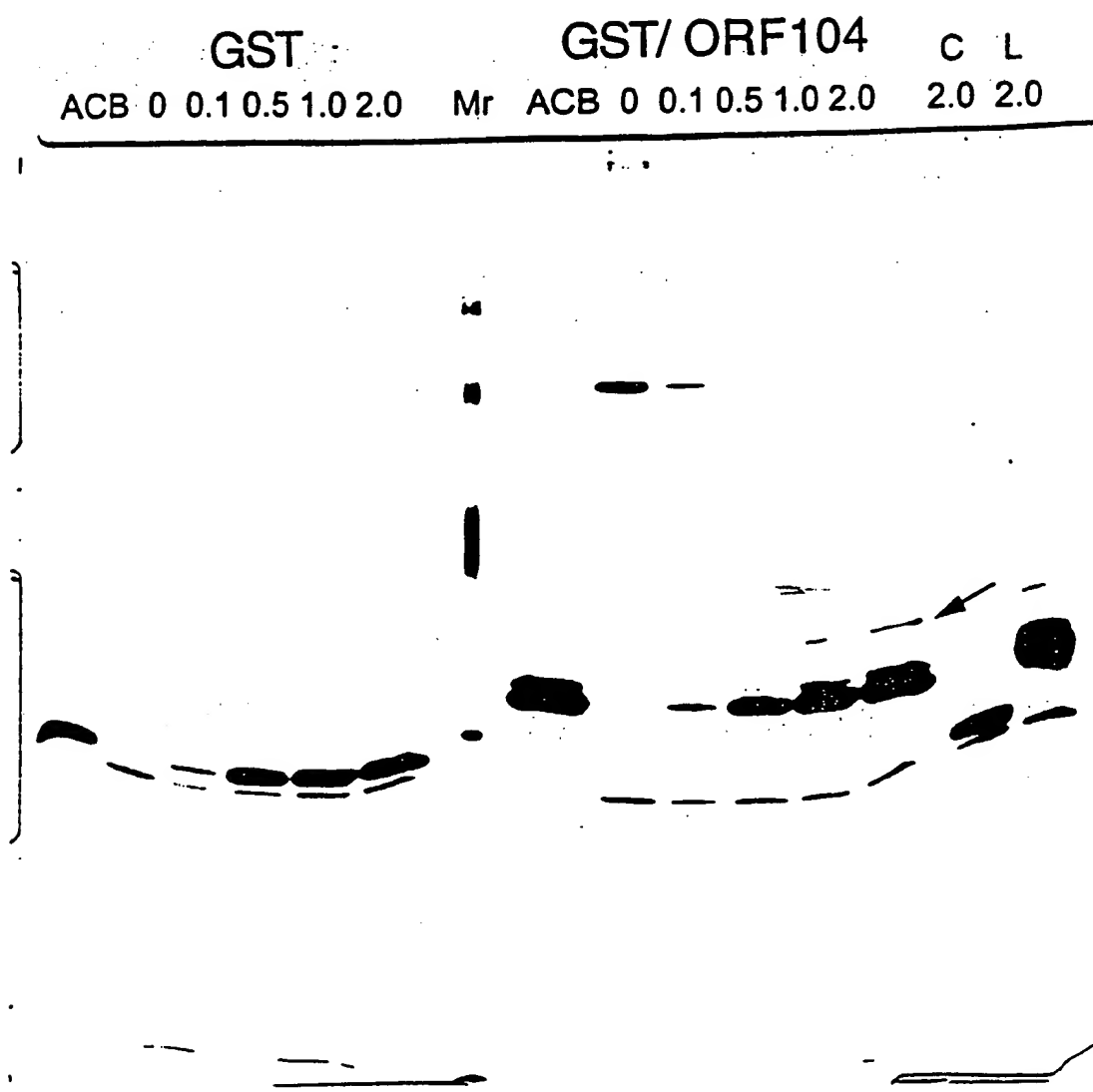
Fig. 10

Figure 11

i) Tryptic peptide mass spectrum of interacting protein (1% Triton X-100 elute)

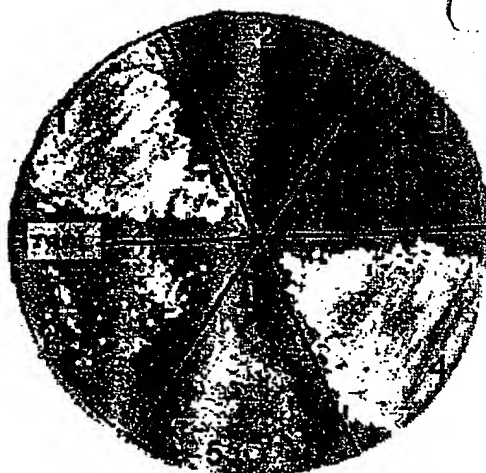ii) Tryptic peptide mass spectrum of interacting protein (1% SDS eluate)

Figure 12

A- *Staphylococcus aureus* genomic DNA

↓ PCR with dnaI-specific primers

EcoRI ▬▬▬▬▬▬▬ BamHI

↓ Digestion with EcoRI and BamHI

EcoRI ▬▬▬▬▬▬▬ BamHI

↓ Subcloning into pGADT7 vector

pGAD dnaI
8.8 kb

B- Phage 77 DNA

↓ PCR with 77ORF104-specific primers

BamHI ▬▬▬▬▬▬▬ PstI

↓ Digestion with BamHI and PstI

BamHI ▬▬▬▬▬▬▬ PstI

↓ Subcloning into pGBKT7 vector

pGBK 77ORF104
7.5 kb

C-

No transcription

Reporter genes: LacZ, *HIS3* and *ADE2*

No transcription

Reporter genes: LacZ, *HIS3* and *ADE2*

Transcription

Reporter genes: LacZ, *HIS3* and *ADE2*

Fig 12 D & E

SD plate without Trp and Leu   SD plate without Trp, Leu, His and Ade

1) pGBKT7-53 and pGADT7-T
2) pGBKT7-53 and pGAD dna I
3) pGBK77ORF104 and pGADT7-T
4) pGBKT7-LAM and pCL1
5) pGBK77ORF104 and pGAD dna I
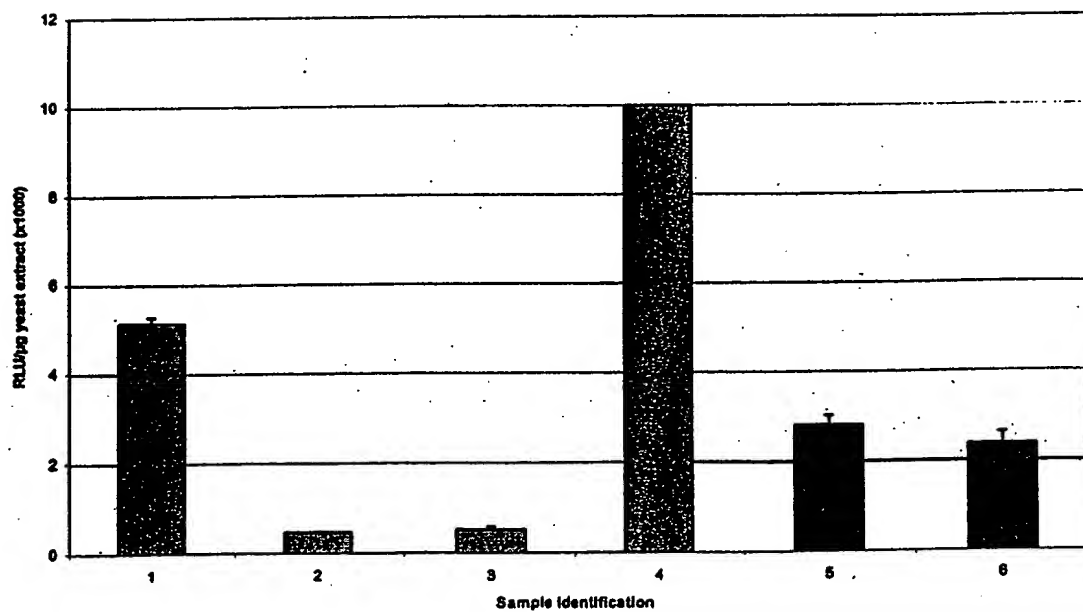6) pGBK dna I and pGAD77ORF104

E)

Luminescent ß-Galactosidase Assay

Fig. 13

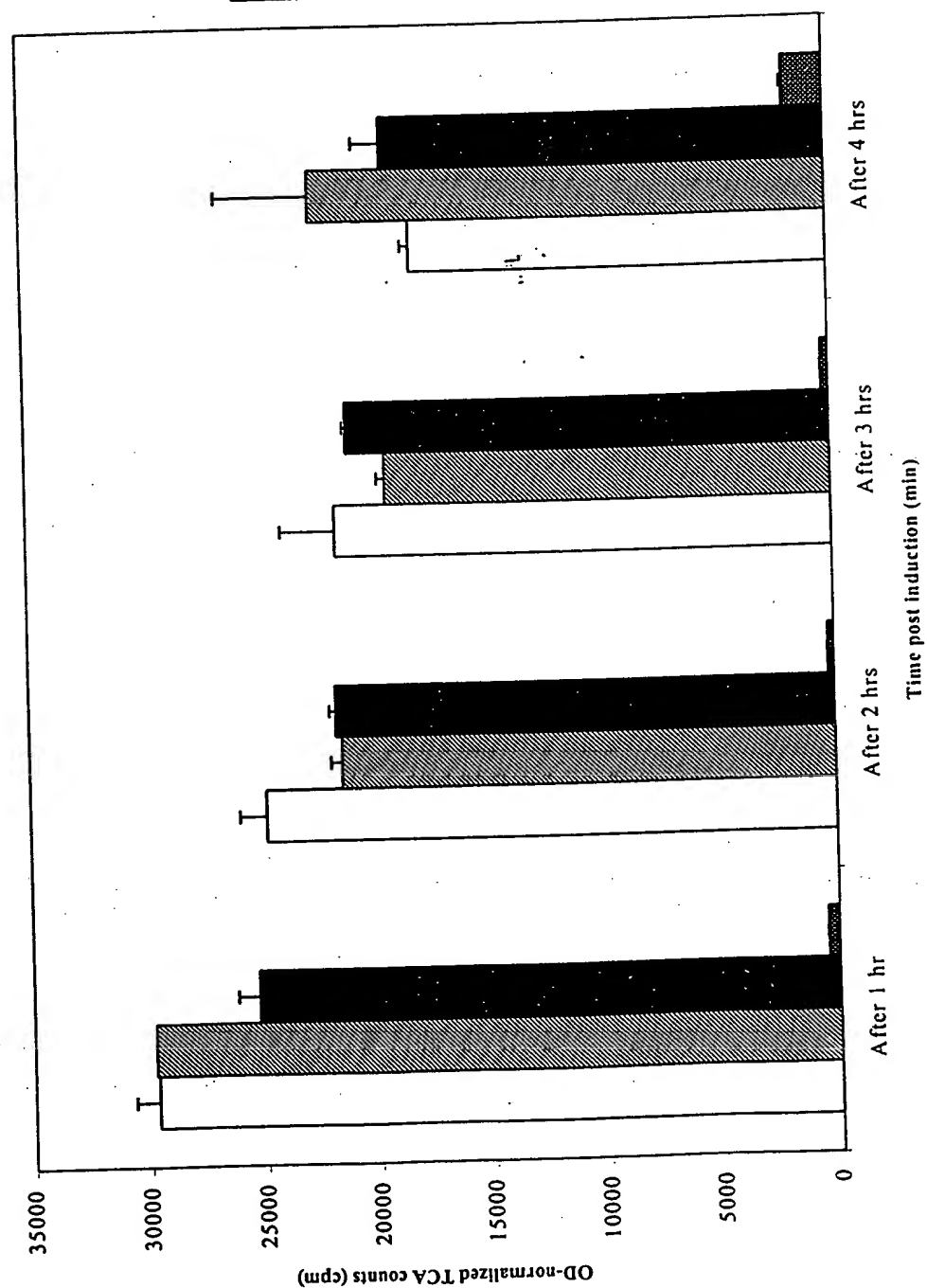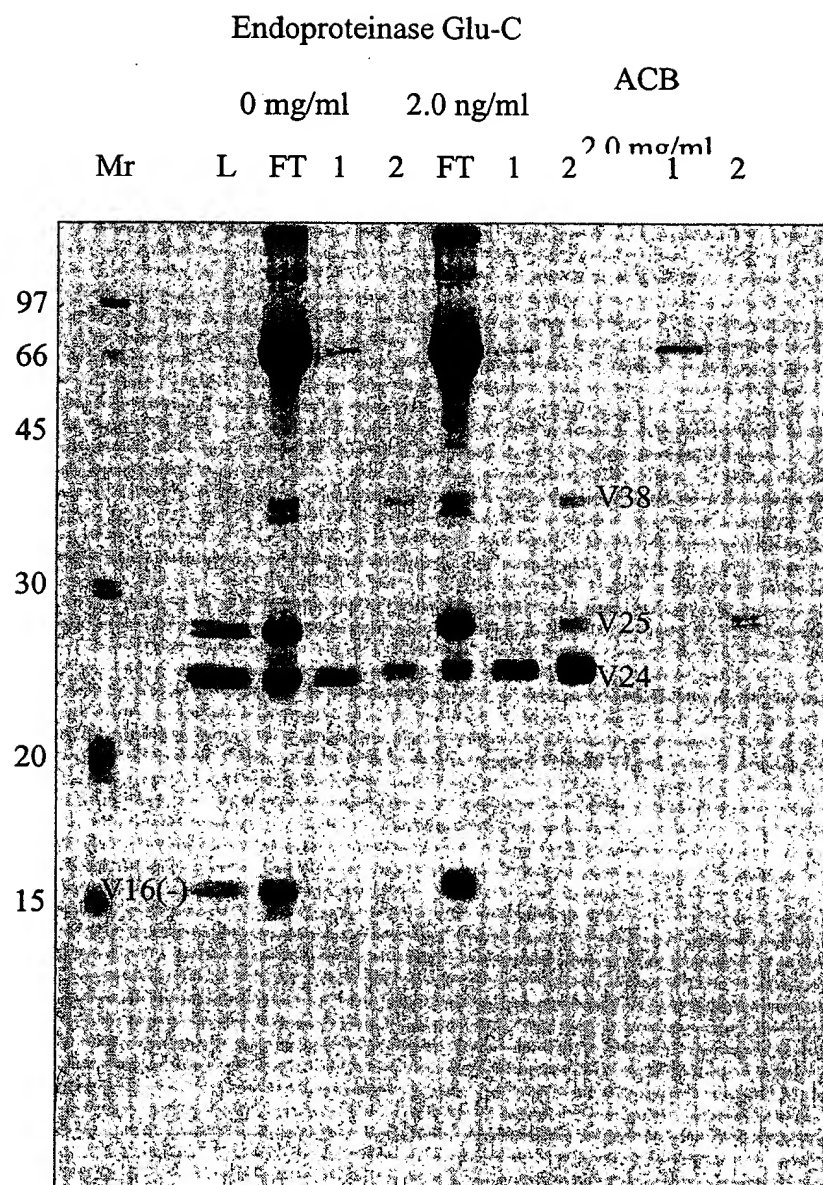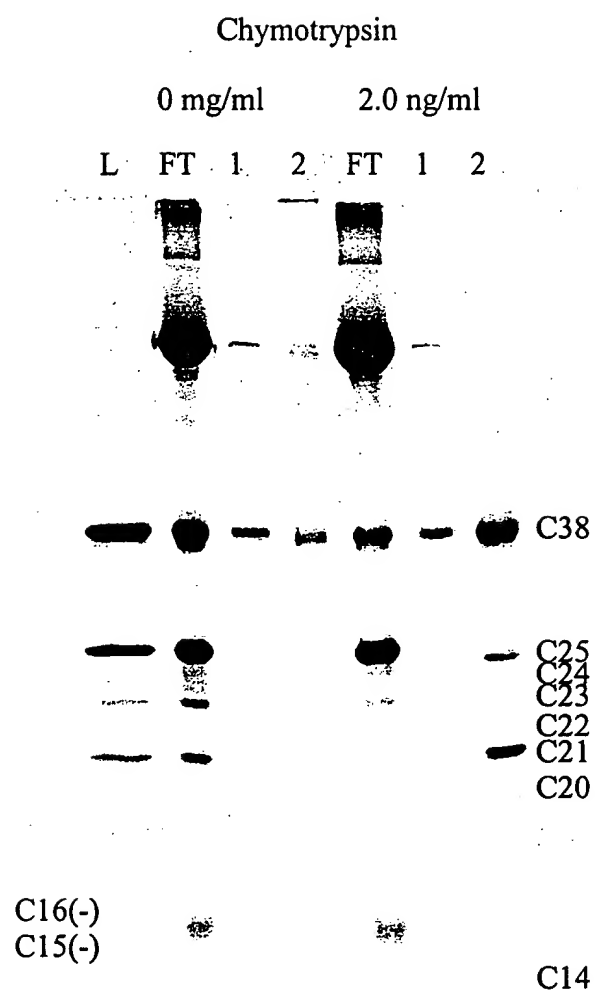Effect of 77ORF 104 expression on 3H-Thymidine incorporation

Legend:
- ☐ Non killer ORF, no induction
- ▨ Non killer ORF, induction
- ■ 77pTORF104, no induction
- ▩ 77pTORF104, induction

X-axis: Time post induction (min)
After 1 hr, After 2 hrs, After 3 hrs, After 4 hrs

Y-axis: OD-normalized TCA counts (cpm)
0, 5000, 10000, 15000, 20000, 25000, 30000, 35000

FIGURE 14A

Endoproteinase Glu-C

ACB

	0 mg/ml		2.0 ng/ml	2.0 mg/ml
Mr	L FT 1 2	FT 1 2	1 2

FIGURE 14B

Chymotrypsin

0 mg/ml   2.0 ng/ml

L   FT   1   2   FT   1   2

C38

C25
C24
C23
C22
C21
C20

C16(-)
C15(-)

C14

FIGURE 14C

Amino acid residues corresponding to interacting partial
proteolytic fragments.

Protease	Proteolytic fragment ID (from Fig. 14A, B)	ID of SEQ ID NO: 2 fragment interacting with 77ORF104	
		from amino	to carboxyl
Endoproteinase Glu-C	V24	117	313
	V24	119	313
Chymotrypsin	C38	12	313
	C25	83	313
	C24	77	305
	C23	77	304
	C22	116	313
	C21	131	313
SEQ ID NO: 2	Complete	1	313

FIGURE 15

SEQ ID NO: 16
>*S.aureus* dnaI :amino acid 150-313
AADDICTAITNGEQVKGLYLYGPFGTGKSFILGAIANQLKSKKVRSTIIYLPEFIRTLKG
GFKDGSFEKKLHRVREANILMLDDIGAEEVTPWVRDEVIGPLLHYRMVHELPTFFSSNFD
YSELEHHLAMTRDGEEKTKAARIIERVKSLSTPYFLSGENFRNN
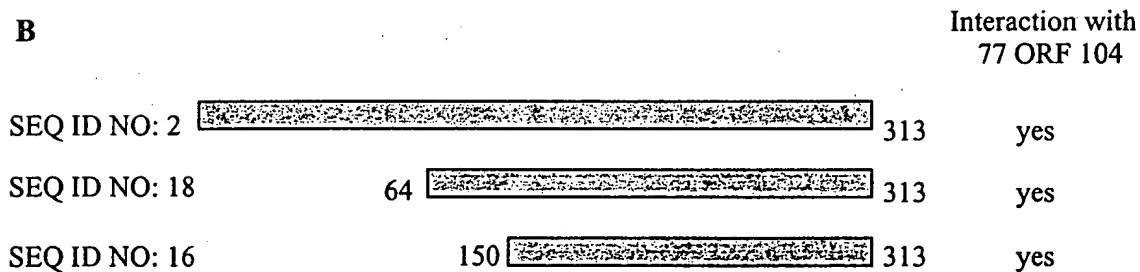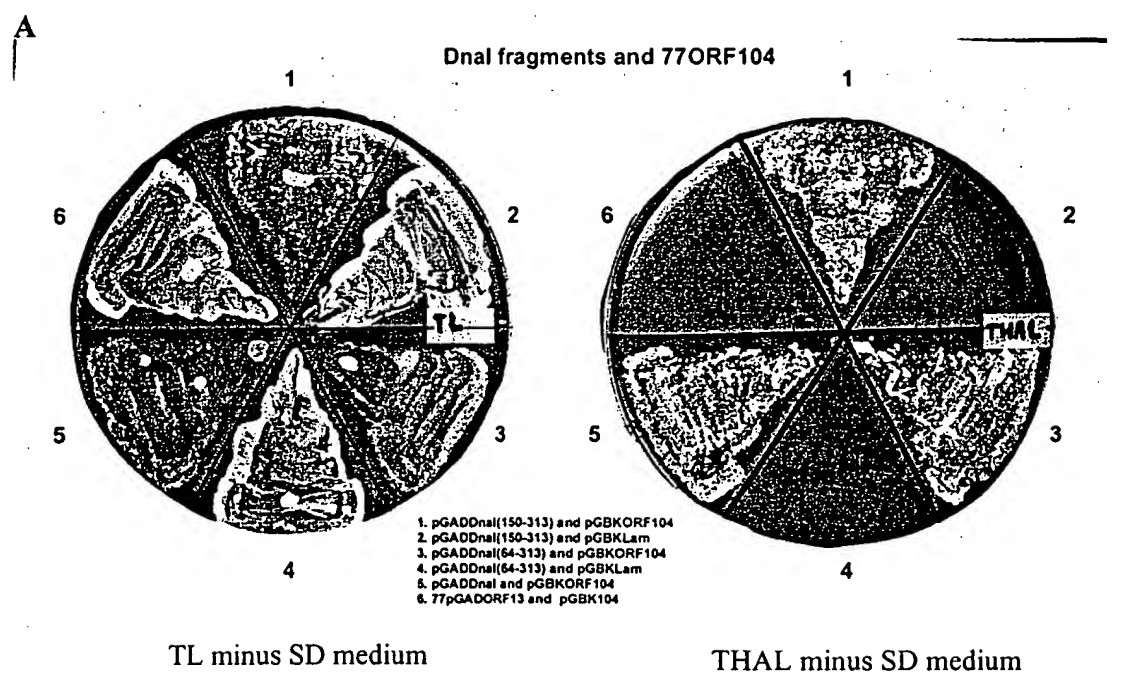
SEQ ID NO: 17
>*S.aureus* dnaI : nucleotide 448-942
gcagcagatgatatttgtacagcaataactaatggggaacaagtgaaaggcctttacctt
tatggtccatttgggacaggtaaatctttattctaggtgcaattgcgaatcagctcaaa
tctaagaaggtacgttcgacaattatttatttaccggaatttattagaacattaaaaggt
ggctttaaagatggttcttttgaaaagaaattacatcgcgtaagagaagcaaacatttta
atgcttgatgatattggggctgaagaagtgactccatgggtgagagatgaggtaattgga
cctttgctacattatcgaatggttcatgaattaccaacattctttagttctaattttgac
tatagtgaattggaacatcatttagcgatgactcgtgatggtgaagagaagactaaagca
gcacgtattattgaacgtgtcaaatctttgtcaacaccatacttttatcaggagaaaat
ttcagaaacaattga

SEQ ID NO: 18
>*S.aureus* dnaI :amino acid 64-313
YKDQQKHYDGHKFADCPNFVKGHVPELYVDNNRIKIRYLQCPCKIKYDEERFEAELITSHH
MQRDTLNAKLKDIYMNHRDRLDVAMAADDICTAITNGEQVKGLYLYGPFGTGKSFILGAI
ANQLKSKKVRSTIIYLPEFIRTLKGGFKDGSFEKKLHRVREANILMLDDIGAEEVTPWVR
DEVIGPLLHYRMVHELPTFFSSNFDYSELEHHLAMTRDGEEKTKAARIIERVKSLSTPYF
LSGENFRNN

FIGURE 16

A

Dnal fragments and 77ORF104

1. pGADDnal(150-313) and pGBKORF104
2. pGADDnal(150-313) and pGBKLam
3. pGADDnal(64-313) and pGBKORF104
4. pGADDnal(64-313) and pGBKLam
5. pGADDnal and pGBKORF104
6. 77pGADORF13 and pGBK104

TL minus SD medium   THAL minus SD medium

B

		Interaction with 77 ORF 104
SEQ ID NO: 2	313	yes
SEQ ID NO: 18	64 — 313	yes
SEQ ID NO: 16	150 — 313	yes